

3406

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AAGCTTAAGGAGGTTAATCG ATG AAA AAA ACT GCT ATC GCT ATC GCT GTT

H A C met

i f RBS

n l a

3 2 1

GCT CTG GCT GGT TTC GCT ACT GTT GCT CAG GCG GCG CCG AGA TCT

aIa N B

a r 1

1 2

a s

1 a

AAA CAG GAA TTC GAG CTC GGT ACC CGG GGA TCC TCT AGA GTC GAC

E S K X B X S

C a P m a b a

O c h a m a 1 1

I 1 1 1 1 1 1

CTG CAG GCA TGC

P S |

S P |

t h |

1 1 |

3557

cI857

P_R

7 NUCLEOTIDES

ClaI

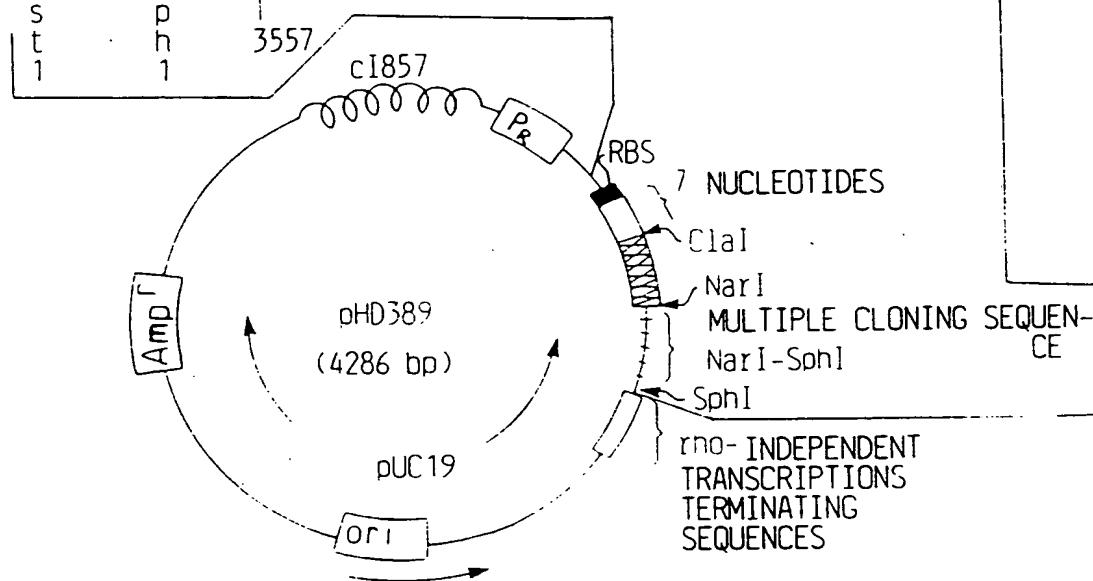
NarI

NarI-SphI

SphI

MULTIPLE CLONING SEQUE-
NCE

rho-INDEPENDENT
TRANSCRIPTIONS
TERMINATING
SEQUENCES



SIGNAL PEPTIDE FOR THE
SEQUENCE FROM OmpA

RBS = RIBOSOMAL AGGAGG
BINDING SEQUENCE

P_R = "RIGHT" PROMOTOR FROM COLIPHAGE λ

cI857 THE GENE FOR A HEAT-SENSITIVE REPRESSOR-PROTEIN FROM COLIPHAGE λ

MULTIPLE CLONING SEQUENCE

NarI
BglII
EcoRI
SacI
KpnI
XmaI
BamHI
XbaI
SalI
PstI
SphI

UNIQUE
CLEAVING
SITES

FIG. 1 PLASMA pHD 389. THE RIBOSMAL
BINDING-SEQUENCE (EMPHASIZED WITH
A FULL LINE), THE SEQUENCE FOR SIGNAL PEPTIDE FROM ompA
(FROM E.coli) (DOTTED LINE) AND RECOGNITION SEQUENCE FOR
SEVERAL RESTRICTION ENZYMES ARE SHOWN.

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PROTEIN LG

GCGGTAGAAATAAGAACACCCAGAAACTGATTCAAGAAGAACAGTA 60
 AlaValGluAsnLysGlugluThrProGlutProGluThrProGluVal 20

ACAATCAAAGCTAACCTAAATCTTGCCTAAATGGAAAGCACACAAACTGCAGATACTTGCGTATGCAGATACCTTTGAAGAAAGACAAT 120
 ThrIleLysAlaAsnLeuIlePheAlaAsnGlySerThrGlnThrAlaGluPheLysGly 40

ACATTTGAAAAGCAACATCAGAGCTTATGCCTTAAATTTGAAGAAAGACAAT 180
 ThrPheGluLysAlaThrSerGluAlaTyrAlaTyrAlaAspThrLeuLysLysAspAsn 60

GGAGAATACTGTAGATGTTGCAGATAAGGTATACTTTAAATATAATTGCTGGA 240
 GlyGlutYrrThrValAspValAlaAspLysGlyTyrThrLeuAsnIleLysPheAlaGly 80

AAAGAAAAACACCAAGAACCAAAAGAACAGTTACTATTAAAGCAAACCTTAATCTAT 300
 LysGluLysThrProGlucGluProLysGluGluValThrIleLysAlaAsnLeuIleTyr 100

GCAGATGGAAAAACACCAAGCAGAAATCAAGGAACATTGAAAGAACAGCAGAA 360
 AlaAspGlyLysThrGlnThrAlaGluPheLysGlyThrPheGluAlaThraAglu 120

FIG. 2
(CONT.)

v v v v v v v v v v v v
 GCATACAGATATGCCAGATGCAATTAAAGAACAAATGGAGAATATACTAGTAGACGTTGCA
 AlaTyrArgTyrAlaAspAlaLeuLysIleAspAsnGlyGlutYrThrValAspValAla
 420
 140

v v v v v v v v v v v v
 GATAAAGGTACTTAAATTAATTTGCTGGAAAGAAAAAACACCGAAAGAACACCA
 AspLysGlyTyrThrIleAsnIleLysPheAlaGlyLysGluLysThrProGluGluPro
 480
 160

v v v v v v v v v v v v
 AAAGAAGTACTTAAAGCAAACCTTAATCTATGCAGATGGAAAAAACACAAACAGCA
 LysGluValThrIleLysAlaAsnLeuIleTyrAlaAspGlyLysThrGlnThrAla
 540
 180

v v v v v v v v v v v v
 GAATTCAAAGGAACCATTTGAAGAACAGCAAGCATACTAGATATGCTGACTTATA
 GluPheLysGlyThrPheGluGluAlaThrAlaGluAlaTyrArgTyrAlaAspLeuLeu
 600
 200

v v v v v v v v v v v v
 GCAAAAGAAAATGGTAAATTACAGTACGACGATAAAGGTTACTTTAAATATT
 AlaLysGluAsnGlyLysTyrThrValAspValAlaAspLysGlyTyrThrLeuAsnIle
 660
 220

v v v v v v v v v v v v
 AACTTAATCTATGCCAGATGGAAAAACACTCAAACAGCAGACTTCAAAAGGAACATTTGCAGAA
 AsnLeuIleTyrAlaAspGlyLysThrGlnThrAlaGluPheLysGlyThrPheAlaGlu
 720
 240

v v v v v v v v v v v v
 AACTTAATCTATGCCAGATGGAAAAACACTCAAACAGCAGACTTCAAAAGGAACATTTGCAGAA
 AsnLeuIleTyrAlaAspGlyLysThrGlnThrAlaGluPheLysGlyThrPheAlaGlu
 780
 260 FIG. 2
 (CONT.)

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<pre> v v v v v v AAACTTATTAAATGGTAAACATTGAAAGGGAAACAACTACTAAAGCAGTAGACGCA LysLeuValIleAsnGlyLysThrLeuLysThrLysAlaValAspAla </pre>	<pre> v v v v v v GAAACTGCAGAAAAGCCTCAAACAAATAACGCTAACGACAAACGGTGTTGATGGTGTTGG GlutHalaGluLysAlaPhelysGlnTyrAlaAsnAspAsnGlyValAspGlyValTrp </pre>
1200 400	1260 420

FIG. 2

V V V V
 ACTTATGATGGCACTAAGACCTTACGGTAAC TGAAATGTAATAA 1308
 Thr Tyr Asp Asp Al a Thr Lys Thr Phe Thr Val Thr Glu Met - - 434



FIG. 2

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FIG. 3 SCHEMATIC OVERALL VIEW OF THE PRODUCTION OF PROTEIN L

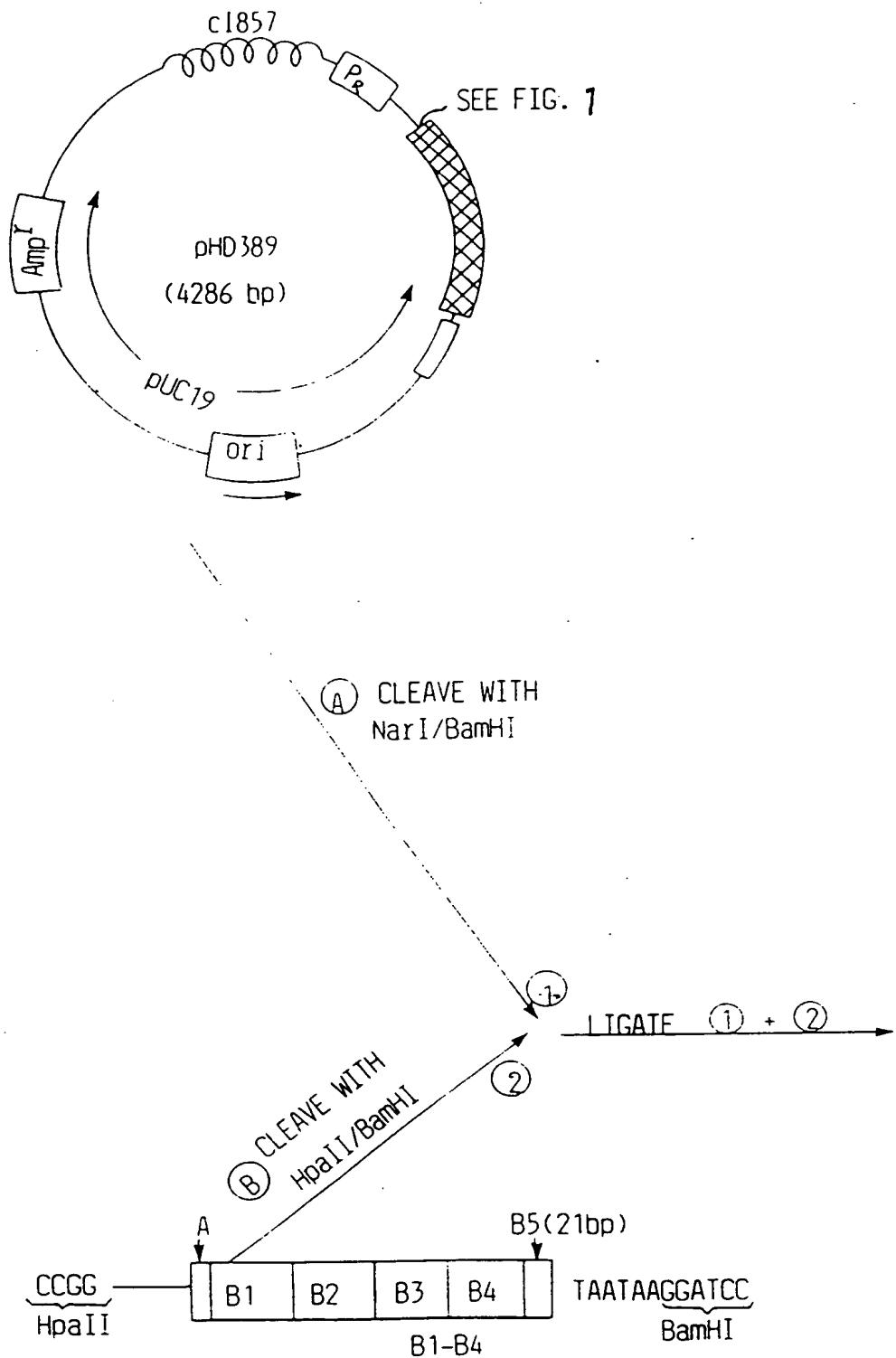


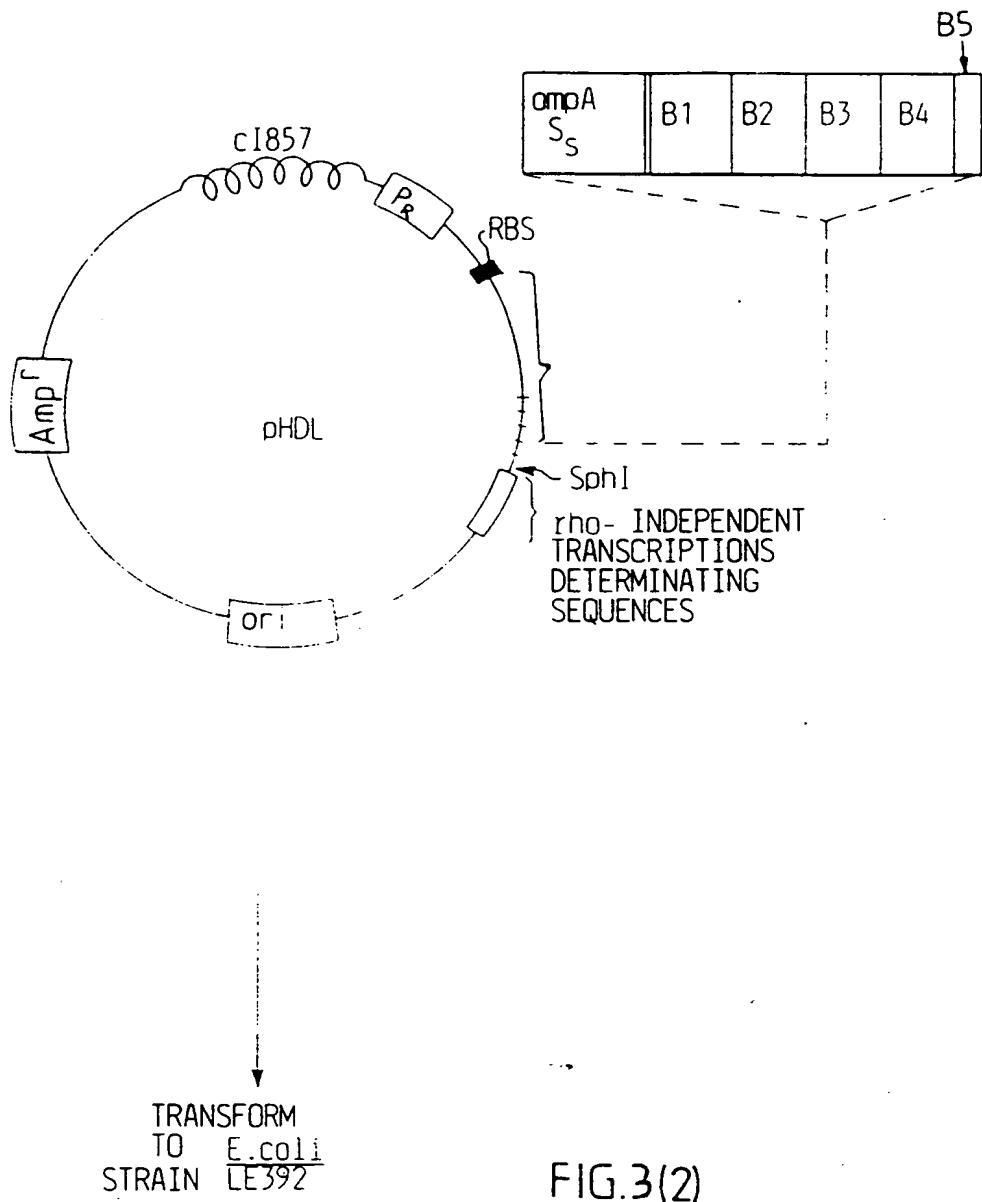
FIG. 3(1)

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WO 93/22342

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FIG.4

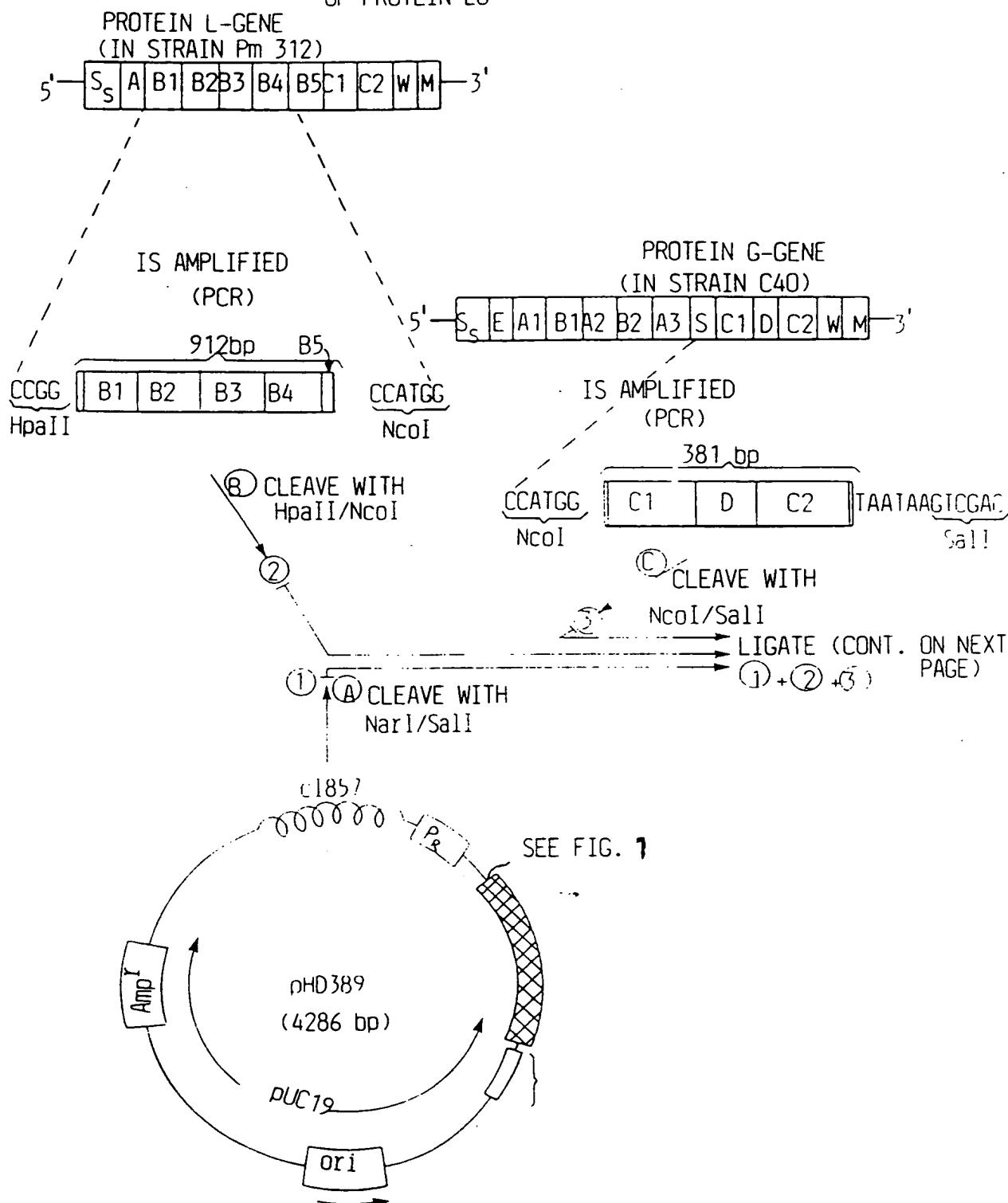
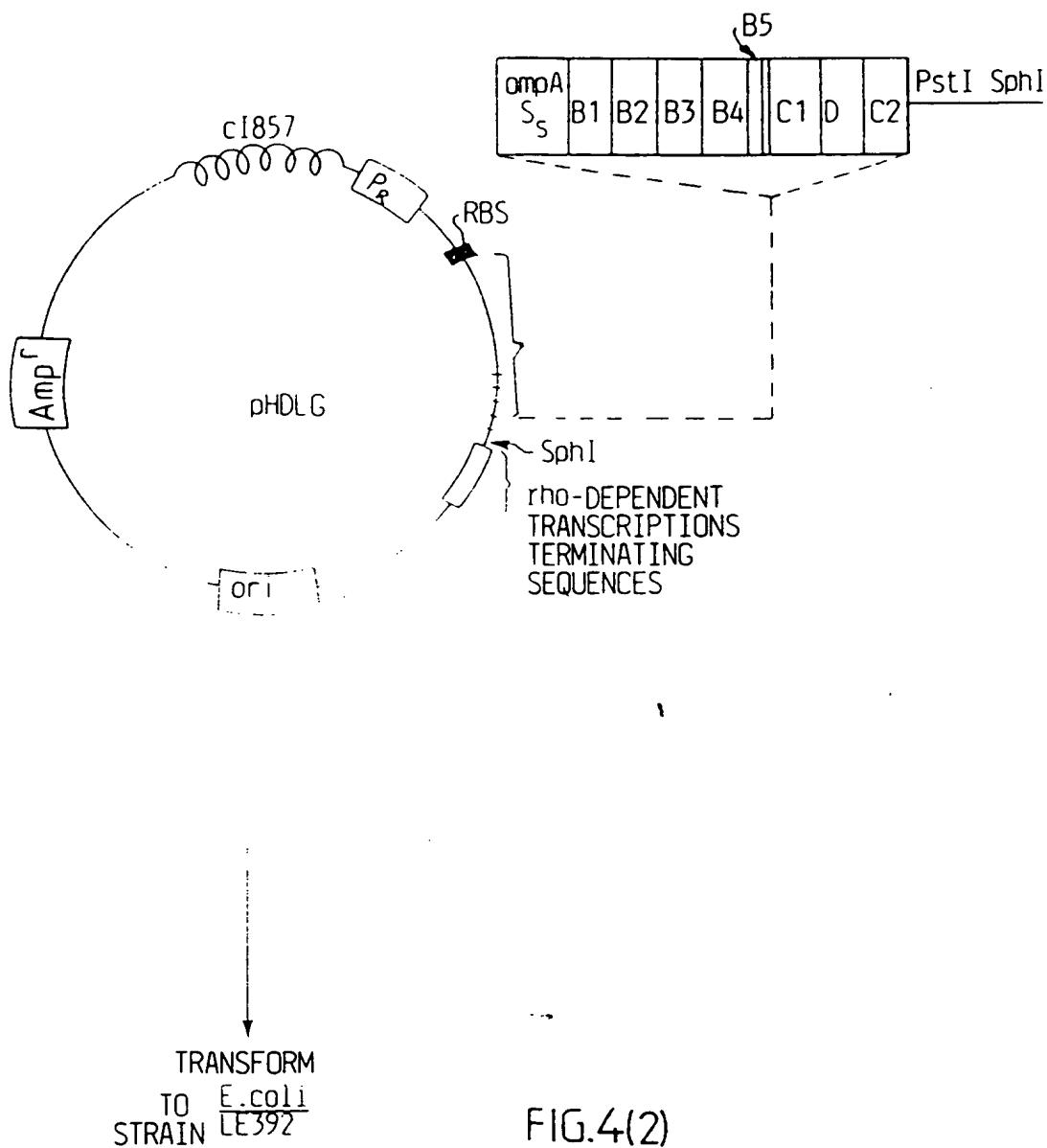
SCHEMATIC OVERALL VIEW OF PRODUCTION
OF PROTEIN LG

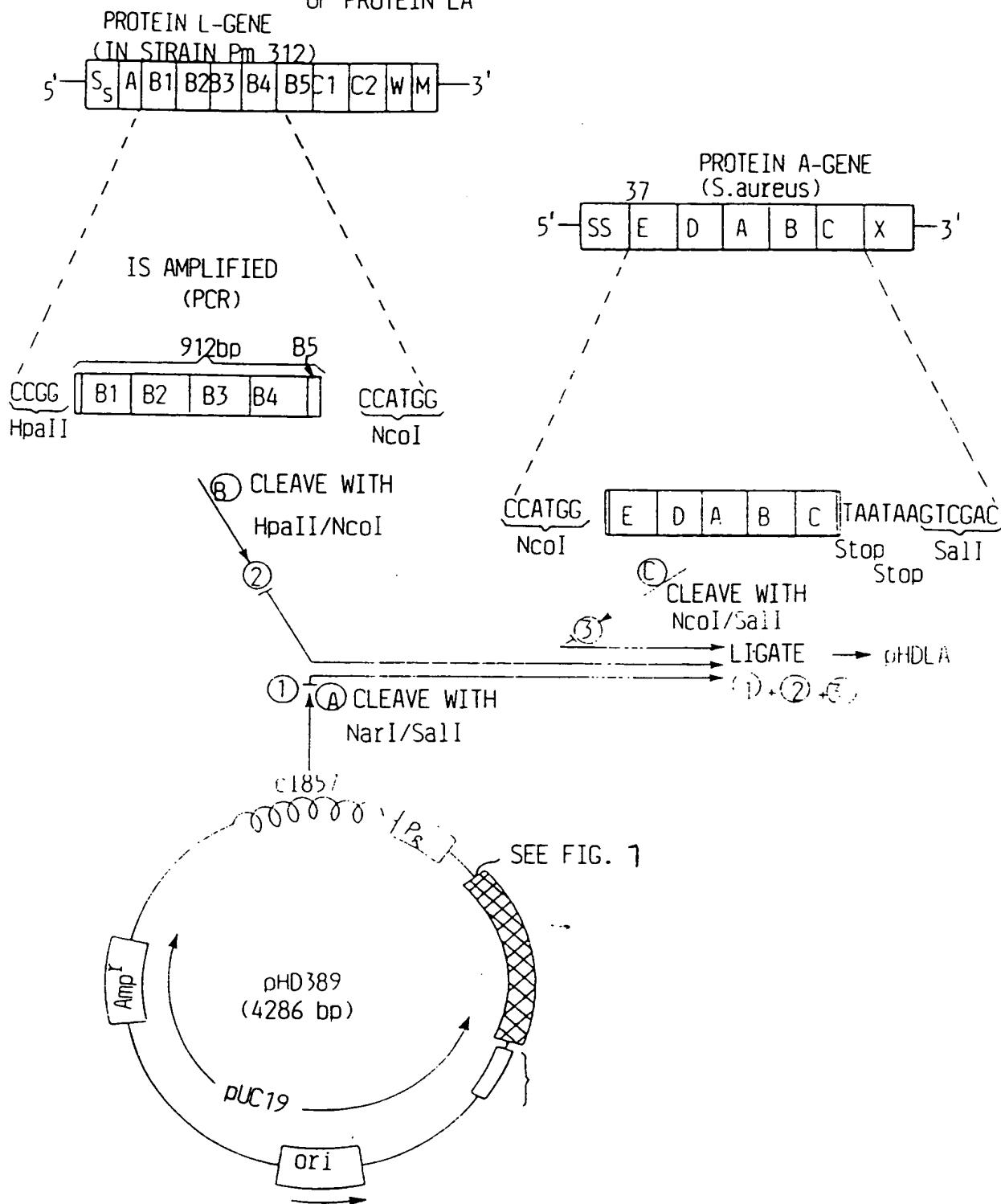
FIG4(1)

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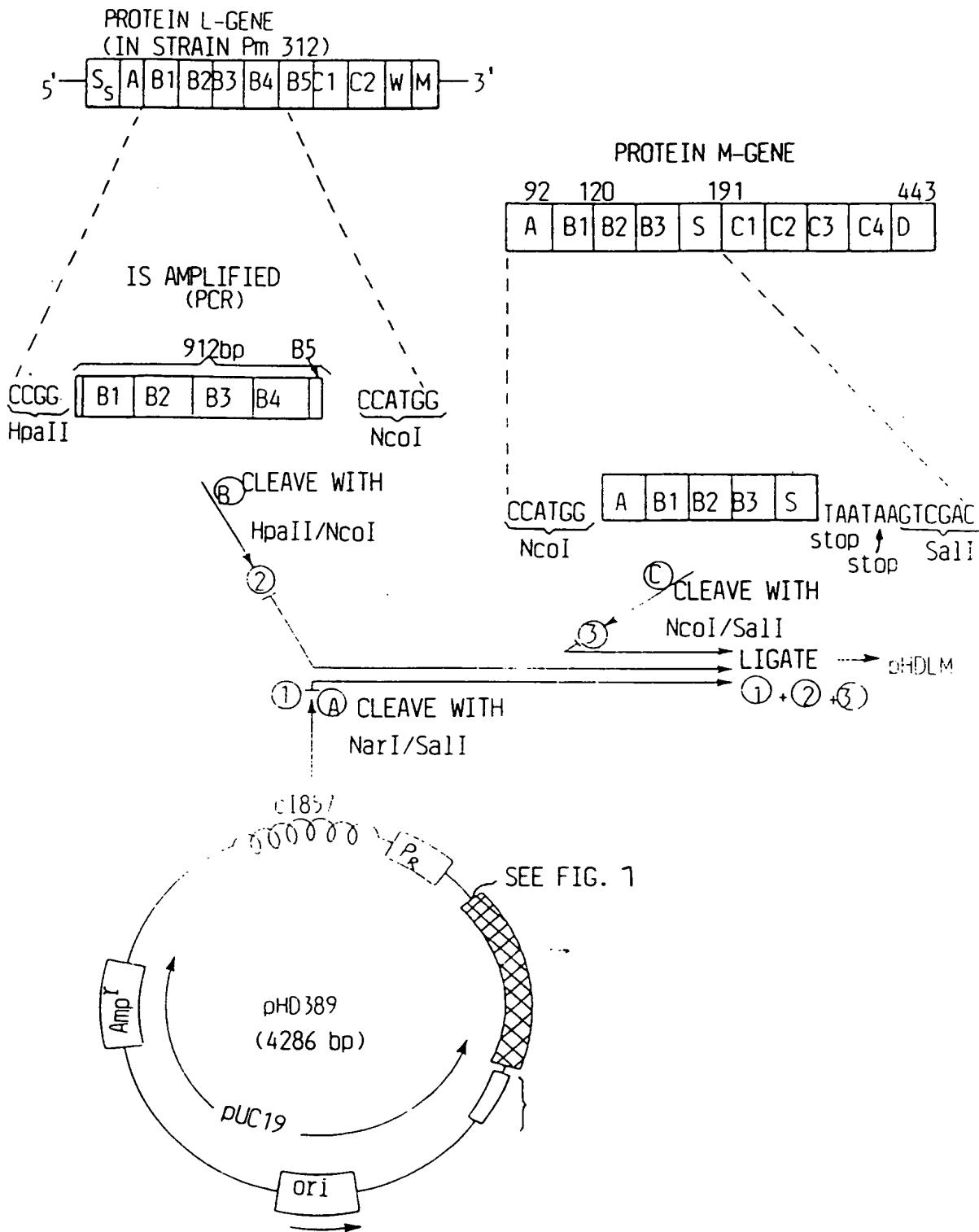
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FIG. 5c

SCHEMATIC OVERALL VIEW OF THE PRODUCTION
OF PROTEIN LA

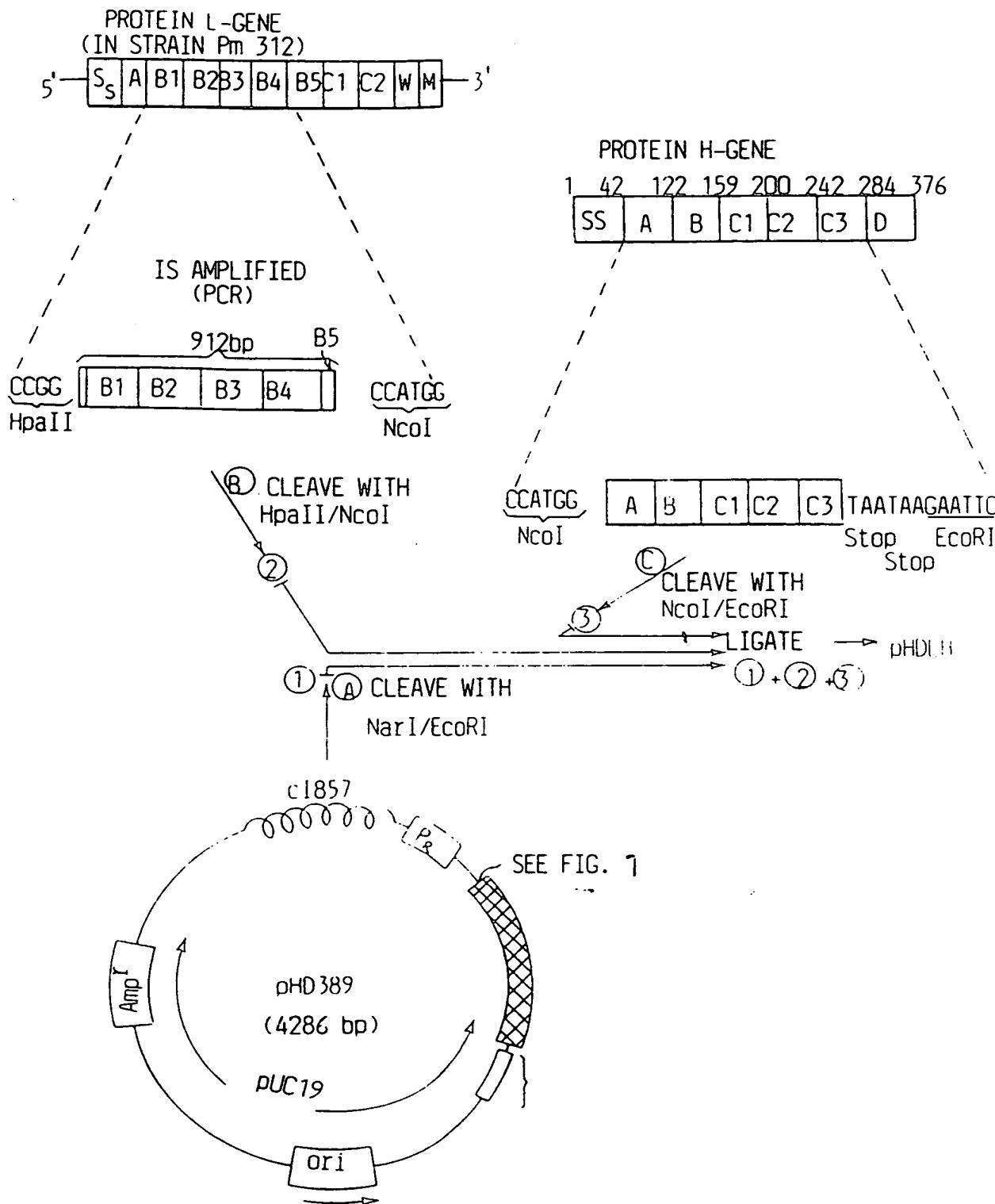
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FIG.5b SCHEMATIC OVERALL VIEW OF THE PRODUCTION OF PROTEIN LM



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FIG. 5 C SCHEMATIC OVERALL VIEW OF THE PRODUCTION OF PROTEIN LH



	PROTEIN A						
1	37	93	154	212	270	328	524
	Ss	E	D	A	B	C	X

	PROTEIN G														
1	34		141	216	267	303	373	443	498	593					
	Ss	E	A1	B1	A2	B2	A3	S	C1	D1	C2	B	C3	W	M

117 192 291 358 428 568

	PROTEIN H								
1	42		122	159	200	242	284	376	
	Ss	A	B	C1	C2	C3	D		

B3 (148-153)

	M1 PROTEIN									
1	A	B1	B2	S	C1	C2	C3	C4	D	

92 120 154 191 233 275 318 339 443

FIG. 6

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AACGGTGTAACTCCTAGGGAAAGTTATAGAGATCTTGCAGCAAAACAAATCCCCGAAATA
 AsnGlyAspGlyAsnFromArgLysValIleGluValIleGluAspLeuAlaAlaAsnAsnFroAlaIle 60
 20

CAAATAATACGTTACGTACGGAAACAAAGGACTTAAGAAGCCGAGATTAGAGAATGCCAATG
 GluValAlaGlyAspGlyAsnLysAspLeuIleGluAsnAlaArgLysAlaAsnAlaMet 120
 40

GAAGGTTGCAGGAAGGAGATTAGAGAGACTGAAAGAACCTTGAAAGCAAAACAAGGCCCTTA
 GluValAlaGlyAspGlyAsnLysAspLeuIleGluAlaGluGluLysAlaLysGinAlaLeu 180
 60

GAAGGACCAGCGTAAAGATTAGAAACTAAATTAAAGAAACTACAAACAAAGACTATGACTTA
 GluAspGlyAsnArgLysAspLeuGluThrLysLeuLysGluLysGluGlnGlnAspTyrAspLeu 240
 80

GCAAAAGGAAATCAACAAAGTTGGGATAGACCAAGGAAAGACTTGAAGAGAGTTAGAAAGAGAAAAAG
 AlalysGluSerThrSerTrpAspArgGinArgLysGluLysGluLysGluLysLys 300
 100

GAAGGCTCTTGAATTAGCGGATAGACCCAGGCAAGGTGGGACTTACCCAGGCTTACCGCTTTA
 GluAlaLeuGluLeuAlaIleAspGlnAlaSerArgAspTyrHisArgAlaThrAlaLeu 360
 120

GAAAAGGAGTTAGAAAGAGAAAAAGAAAGCTCTTGAATTAGCCGATAAGCAGAACGTCAG
 GluLysGluLysGluLysGluLysGluLysGluLysGluLysGluLysGluLys 420
 140

GACTATAATAGAGCTAACGCTCTAGAAAGAGTTAGAAACCGATTACTAGAGAACAAAGAG
 AspTyrAsnArgAlaAsnValleGluGluGluGluThrIleThrArgGluGluGlu 480
 160

ATTAAATCGTAAATCTTCTTAGGCCAAACTGCAACTTGAAACTTCAACTTCTCATCTGAAAAAA
 IleAsnArgAsnLeuLeuGlyAsnAlaLysLysGluLysGluLysSerGluLys 540
 180

FIG. 7 (CONT.)

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GAGCAGGCTAACGATCGAAAAGSCAAACATT
 GluGlnLeuThrIleGluLysAlaLysLeuGluGluGluLysGlnIleSerAspAlaSer 190 600
 CGTCAAAGCCTTCGTGACTTGACGCCATCACGTTGAAAGCTAAGAAACAGGTTGAAAAA
 ArgGlnSerLeuArgArgAspLeuAspAlaSerArgGluAlaLysLysGlnValGluLys 220 660
 GATTTAGCAAAACTTGACTTGCTGAATTAAAGGTTAAAGAACAAATCTCAGAC
 AspLeuAlaAsnLeuThrAlaGluLysAspLysValLysGluAspLysGlnIleSerAsp 240 720
 GCAAGGCCGTCAACGGCTTCGCCGTGACTTGACGCATCACGTTGAAAGCTAAGAAACAGGTT
 AlaSerArgGlnArgLeuArgArgAspLeuAspAlaSerArgGluAlaLysLysGln 780

FIG. 7 (CONT.)

Amino acid sequence and nucleic acid sequence for protein M1, IgG-binding somewhere between amino acid 1-190.

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GAAAAGATTAGCAAACTTGACTTGAACTTGTGAACTTGATTAAGGTTAAAGAAGAAAAACAAATC
 GluLysAspLeuAlaAsnLeuThrAlaGluLeuAspLysValLysGluGluLysGinile 840
 290

TCAGACGCCCTCAACGGCTTCGCGGTGACTTGCGCATCACGGTGAAGCTAAGGAAA
 SerAspAlaSerArgGluArgAspLeuArgArgLeuArgArgLys 900
 300

CAAGTTGAAAGCTTTAGAAGCAAAACAGCAAATTAGCTGCTCTGAAACTAAC
 GinValGluLysAlaLeuGluGluAsnSerLysLeuAlaAlaLeuGluLysLeuAsn 960
 320

AAAGAGCTTGAAGAAAGCAAAAGAAATTAAACAGAAAAAGGAAAGCTGAAACTACAAGGCAAA
 LysGluLeuGluGluSerLysLeuThrGluLysGluLysAlaGluLeuGluAlaLys 1020
 340

CTTGAAGCAAGCAAAAGCACTCAAAGAACAAATTAGCGAAACAAAGCTGAAAGAAACTCGCA
 LeuGluAlaGluAlaLysAlaLeuLysGluGluLeuAlaLysGinAlaGluLysLeuAla 1080
 360

AAACTAAGAGCTGGAAAAAGCATEAGACTCACAAACCCCTGATAACAAACCCGAAACAAA
 LysLeuArgAlaGluLysAlaSerAspSerGlnThrProAspThrLysProGlyAsnLys 1140
 380

GCTGTCCAGGTTAAAGCAGGTACAAACCTAACCCAAACCAAGGAAAGCA
 AlaValFroGlyLysGluGlyGlnAlaProGlnAlaGlyThrLysFroAsnGinAsnLysAla 1200
 400

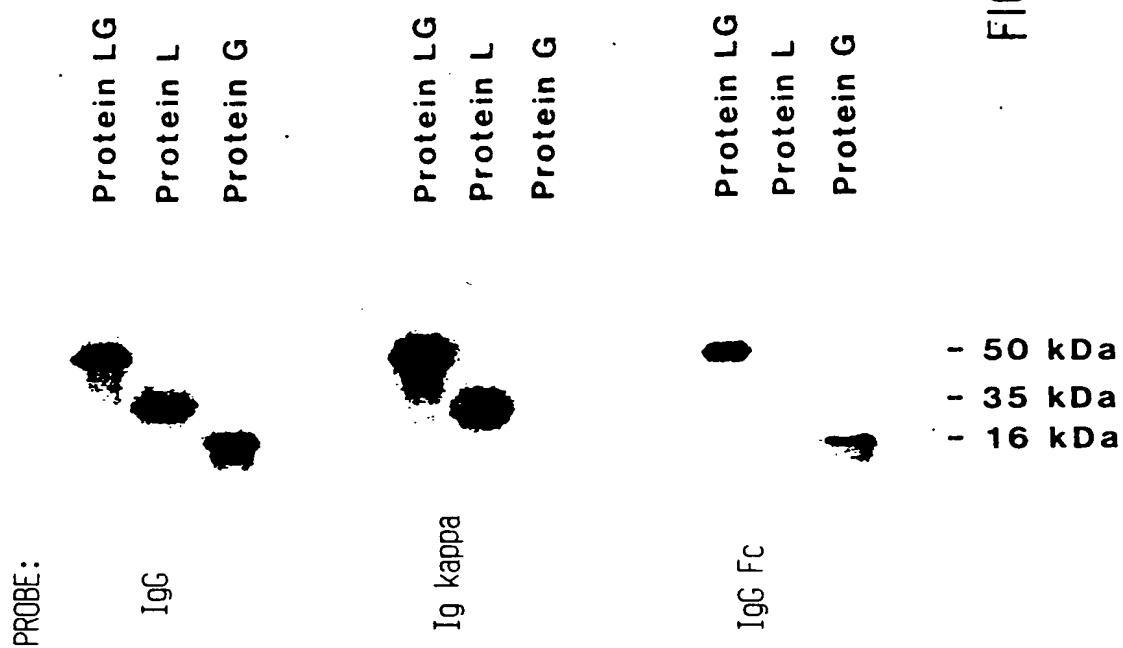
CCAATGAAGGAAACTAAGAGACAGTTACCATCAACAGGTGAAACAGCTAACCCATTCTC
 PrometLysGluThrLysArgGlnLeuProSerThrGlyGluThrAlaAsnProPhePhe 1260
 420

ACAGGGGCCACGGCTTACTGTTATGGCAACAGCTGGAGTAGGCAGTTGTAACACGGCAA
 ThrAlaAlaArgValThrValMetAlaThrAlaGlyValAlaAlaValValLysArgLys 1320
 440

GAAGAAACCTAA
 GluGluAsn 1329
 443

FIG. 7

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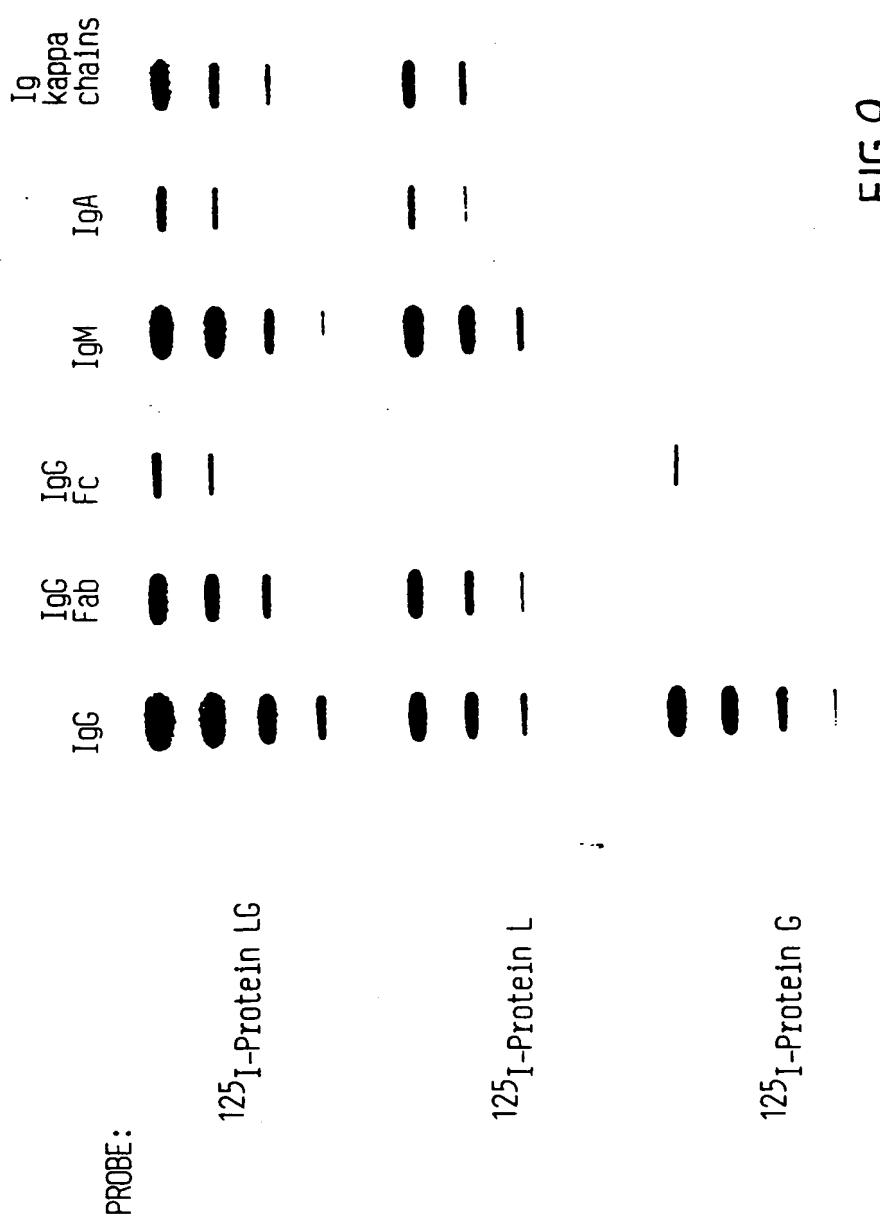


FIG. 9

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